

Email: asimpson@ludwig.org.br
 This sequence was derived from the FARESH/Lick Human Cancer Genome Project. This entry can be seen in the following URL:
 (http://www.ludwig.org.br/scripts/gethtml2.pl?1165&AT2-R65-GN281-010201-013-A0043-2001-02-015&4-1)
 Seq primer: puc 18 forward
 High quality sequence stop: 214.

FEATURES

Location/Qualifiers
 1..214
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="GN0281"
 /seq_stage="Adult"

/note="Organ: placenta_normal; Vector: puc18; Site_1: Sma1; Site_2: Sma1; A mini library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

BASE COUNT 68 a 36 c 88 g 22 t

ORIGIN

Alignment Scores:
 Pred. No.: 0.0989 Length: 214
 Score: 55.00 Matches: 11
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 13 Gaps: 0

US-09-856-070-23 (1-11) x H054475 (1-214)

QY 1 GluLeuMetLeuArgLeuGlnAspTyrGluGlu 11

DB 54 GAGTTCAGCTGGCCCTGGCAATGATGACGAG 91

RESULT 4

B0367833/C

LOCUS B0367833 215 bp mRNA linear EST 21 MAY 2002

DEFINITION B0367833 013-A00 GN0281 Homo sapiens cDNA, mRNA sequence

ACCESSION B0367833

VERSION B0367833.1 GI:21043334

KEYWORDS EST

SOURCE human

ORGANISM

Homo sapiens

Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;

Mammalia, Eutheria, Primates, Catarrhini, Homiidae; Homo.

1 (bases 1 to 215)

DIAS Neto, P., Garcia Correa, P., Verjovski-Almeida, S., Priones, M. P.,

Nagai, M. A., da Silva, W. T., Zapp, M. A., Bordin, S., Costa, F. F.,

Geldman, C. H., Carvalho, A. F., Matsukuma, A., Batista, S., Simpson, D. H.,

Brunstein, A., deoliveira, P. S., Bucher, P., Jongeneel, C. V., O'Hare,

M. J., Soares, F., Brontani, R. R., Reis, L. F., de Souza, S. I. and

Simpson, A. J.

Shotgun sequencing of the human transcriptome with ORF expressed

sequence tags

Proc Natl Acad Sci U S A 97 (7), 3491-3496 (2000)

CONTACT: Simpson A J C

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Brazil

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FAX: +55-11-2707001

EMAIL: asimpson@ludwig.org.br

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Project. This entry can be seen in the following URL:

(http://www.ludwig.org.br/scripts/gethtml2.pl?1165&AT2-R65-GN281-010201-013-A0043-2001-02-015&4-1)

Seq primer: puc 18 forward.

Location/Qualifiers

source

1..215
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="GN0281"
 /seq_stage="Adult"
 /note="Organ: placenta_normal; Vector: puc18; Site_1: Sma1; Site_2: Sma1; A mini library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

BASE COUNT 22 a 91 c 34 g 68 t

ORIGIN

Alignment Scores:
 Pred. No.: 0.0495 Length: 215
 Score: 55.00 Matches: 11
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 14 Gaps: 0

US-09-856-070-23 (1-11) x H0367833 (1-215)

QY 1 GluLeuMetLeuArgLeuGlnAspTyrGluGlu 11

DB 167 GAGTTCAGCTGGCCCTGGCAATGATGACGAG 125

RESULT 5

B0754562

LOCUS B0754562 234 bp mRNA linear EST 15 MAY 2001

DEFINITION B0754562 602710194F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4846630 5'

ACCESSION B0754562

VERSION B0754562.1 GI:14065215

KEYWORDS EST

SOURCE human

Homo sapiens

Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;

Mammalia, Eutheria, Primates, Catarrhini, Homiidae; Homo.

1 (bases 1 to 234)

NIH-MGC http://imgc.ncbi.nih.gov/

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Staudt, Ph D.

Email: rstaedt@nhi.nih.gov

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

cDNA library preparation: Ling Hong/kubin laboratory

cDNA library Arrayed by: the I.M.A.C.R. Consortium (LLNL)

cDNA sequencing by: Incyte Genomics, Inc.

clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: HICM1687 row: 1 column: 23

High quality sequence stop: 234.

Location/Qualifiers

1..234

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone_image="4846630"

/clone_lib="NIH_MGC_48"

/tissue_type="Primary B-cells from tonsils (cell line)"

/lab_host="DH10B (phage-resistant)"

/note="Organ: B-cells; Vector: pOT7; Site_1: XhoI;

Site_2: PstRI; cDNA made by oligo-dT priming.

Directionally cloned into EcoRI/XhoI sites using the

following 5' adaptor: GCCACGAG(C). Size-selected >500bp

for average insert size 1.8kb. Library constructed by Ling

Hong in the laboratory of Robert M. Kubin (University of

California, Berkeley) using ZAP cDNA synthesis kit

(Stratagene) and Superscript II RT (Life Technologies).

Note: this is a NIH_MGC library."

FEATURES

source

1..234
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_image="4846630"
 /clone_lib="NIH_MGC_48"
 /tissue_type="Primary B-cells from tonsils (cell line)"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: B-cells; Vector: pOT7; Site_1: XhoI;
 Site_2: PstRI; cDNA made by oligo-dT priming.
 Directionally cloned into EcoRI/XhoI sites using the
 following 5' adaptor: GCCACGAG(C). Size-selected >500bp
 for average insert size 1.8kb. Library constructed by Ling
 Hong in the laboratory of Robert M. Kubin (University of
 California, Berkeley) using ZAP cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies).
 Note: this is a NIH_MGC library."

US-09-856-070-23 (1-11) x BF804303 (1-279)

Qy 1 GlutMetLeuArgLeuGlnAspTyrGluGlu 11
 Db 124 GAGTTGATGCTGGCGCTGCTAGGACATAGAGGAG 156

RESULT 8

AW845219 281 bp mRNA linear EST 19 MAY 2000
 DEFINITION CM0-CT0012 290699 017 a05 CT0012 Homo sapiens cDNA, mRNA sequence.

ACCESSION AW845219

VERSION AW845219.1 GI:7940736

KEYWORDS EST.

SOURCE human

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 281)

Dias Neto, E., Garcia Correa, P., Verjovski-Almeida, S., Briones, M. R.,

Nagai, M. A., da Silva, W. Jr., Zago, M. A., Bordin, S., Costa, F. F.,

Goldman, G. H., Carvalho, A. F., Matsukuma, A., Haid, G. S., Simpson, D. H.,

Brunstein, A., de Oliveira, P. S., Bucher, P., Jungueiro, C. V., G. Hare

, M. J., Soares, F., Brentani, R. R., Reis, L. F., de Souza, S. J., and

Simpson, A. J.

Shotgun sequencing of the human transcriptome with ORF expressed

sequence tags

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

MEDLINE 20202663

COMMENT Contact: Simpson A.J.G.

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This sequence was derived from the FAPESP/LICR Human Cancer Genome

Project. This entry can be seen in the following URL

(<http://www.ludwig.org.br/scripts/gethtml2.pl?r1=62-CM0-CT0012-290699-017-a05&r2=1949-06-29&t4=1>)

Seq primer: puc 18 forward

High quality sequence start: 10

High quality sequence stop: 280.

FEATURES

Location/Qualifiers

1..281

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone_lib="CT0012"

/dev_stage="Adult"

/note="Organ: colon; Vector: puc18; Site_1: SmaI; Site_2:

SmaI; A mini-library was made by cloning products derived

from ORSTES PCR (U.S. Letters Patent application No. 196

,716 - Ludwig Institute for Cancer Research) profiles

into the pUC 18 vector. Reverse transcription of tissue

mRNA and cDNA amplification were performed under low

stringency conditions."

BASE COUNT 94 a 52 c 105 g 30 t

ORIGIN

Alignment Scores:

Pred. No.: 0.146 Length: 281

Score: 55.00 Matches: 11

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 10 Gaps: 0

US-09-856-070-23 (1-11) x AW845219 (1-281)

Qy 1 GlutMetLeuArgLeuGlnAspTyrGluGlu 11

Db 179 GAGTTGATGCTGGCGCTGCTAGGACATAGAGGAG 211

RESULT 9

BI050028/c

LOCUS

DEFINITION CM2-CM0294-020101-676-c08 CM0294 Homo sapiens cDNA, mRNA sequence.

ACCESSION BI050028

VERSION BI050028.1 GI:14457558

KEYWORDS EST.

SOURCE human

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 294)

Dias Neto, E., Garcia Correa, P., Verjovski-Almeida, S., Briones, M. R.,

Nagai, M. A., da Silva, W. Jr., Zago, M. A., Bordin, S., Costa, F. F.,

Goldman, G. H., Carvalho, A. F., Matsukuma, A., Haid, G. S., Simpson, D. H.,

Brunstein, A., de Oliveira, P. S., Bucher, P., Jungueiro, C. V., G. Hare

, M. J., Soares, F., Brentani, R. R., Reis, L. F., de Souza, S. J., and

Simpson, A. J.

Shotgun sequencing of the human transcriptome with ORF expressed

sequence tags

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

MEDLINE 20202663

COMMENT Contact: Simpson A.J.G.

Laboratory of Cancer Genetics

Ludwig Institute for Cancer Research

Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,

Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome

Project. This entry can be seen in the following URL

(<http://www.ludwig.org.br/scripts/gethtml2.pl?r1=CM2-CM0294-020101-676-c08&t3=2001-01-02&t4=1>)

Seq primer: puc 18 forward

High quality sequence start: 17

High quality sequence stop: 294.

FEATURES

Location/Qualifiers

1..294

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone_lib="CM0294"

/dev_stage="Adult"

/note="Organ: placenta; Vector: puc18; Site_1: SmaI

; Site_2: SmaI; A mini-library was made by cloning

products derived from ORSTES PCR (U.S. Letters Patent

application No. 196,716 - Ludwig Institute for Cancer

Research) profiles into the pUC 18 vector. Reverse

transcription of tissue mRNA and cDNA amplification were

performed under low stringency conditions."

BASE COUNT 34 a 114 c 56 g 90 t

ORIGIN

Alignment Scores:

Pred. No.: 0.156 Length: 294

Score: 55.00 Matches: 11

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 13 Gaps: 0

US-09-856-070-23 (1-11) x BI050028 (1-294)

Qy 1 GlutMetLeuArgLeuGlnAspTyrGluGlu 11

Db 216 GAGTTGATGCTGGCGCTGCTAGGACATAGAGGAG 178

RESULT 10

BF869430

LOCUS

DEFINITION QM0-ET0148-231000-456-d07 ET0148 Homo sapiens cDNA, mRNA sequence.

ACCESSION BF869430

VERSION BF869430.1 GI:12259560

US-09-856-070-23 (1-11) x BF804303 (1-279)

Qy 1 GlutMetLeuArgLeuGlnAspTyrGluGlu 11

Db 179 GAGTTGATGCTGGCGCTGCTAGGACATAGAGGAG 211

KEYWORDS
SOURCE
ORGANISM

REFERENCE
AUTHORS

TITLE

JOURNAL
MEDLINE
COMMENT

FEATURES
source

BASE COUNT
ORIGIN

Alignment Scores:

Score: 0.158 Length: 312
Matches: 11

Percent Similarity: 100.00%
Conservative: 0

Best Local Similarity: 100.00%
Mismatches: 0

Query Match: 100.00%
Indels: 0

DB: 12 Gaps: 0

US 09 856-070-23 (1-11) x RP869430 (1-297)

OY 1 GluLeuMetLeuArgLeuGlnAspTyrGluGlu 11
|||||
Db 124 GAGTTGATGCTGGGCTGCAAGGACTATGAGGAG 156

RESULT 11
LOCUS RP869430
DEFINITION K-EST00004421 S9SN0601 Homo sapiens cDNA clone S9SN0601-44-609 5', mRNA sequence.
ACCESSION RP869430
VERSION RP869430.1 GI:19183495
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo 1 (bases 1 to 312)

KEYWORDS
SOURCE
ORGANISM

REFERENCE
AUTHORS

TITLE

JOURNAL
MEDLINE
COMMENT

FEATURES
source

BASE COUNT
ORIGIN

Alignment Scores:

Score: 0.17 Length: 312
Matches: 11

Percent Similarity: 100.00%
Conservative: 0

Best Local Similarity: 100.00%
Mismatches: 0

Query Match: 100.00%
Indels: 0

DB: 14 Gaps: 0

US-09-856-070-23 (1-11) x RP827086 (1-312)

OY 1 GluLeuMetLeuArgLeuGlnAspTyrGluGlu 11
|||||
Db 218 GAGTTGATGCTGGGCTGCAAGGACTATGAGGAG 250

RESULT 12
LOCUS RP827086
DEFINITION K-EST00004421 S9SN0601 Homo sapiens cDNA clone S9SN0601-44-609 5', mRNA sequence.
ACCESSION RP827086
VERSION RP827086.1 GI:20935634
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo 1 (bases 1 to 358)

KEYWORDS
SOURCE
ORGANISM

REFERENCE
AUTHORS

TITLE

JOURNAL
MEDLINE
COMMENT

FEATURES
source

BASE COUNT
ORIGIN

Alignment Scores:

Score: 0.17 Length: 312
Matches: 11

Percent Similarity: 100.00%
Conservative: 0

Best Local Similarity: 100.00%
Mismatches: 0

Query Match: 100.00%
Indels: 0

DB: 14 Gaps: 0

US-09-856-070-23 (1-11) x RP827086 (1-312)

OY 1 GluLeuMetLeuArgLeuGlnAspTyrGluGlu 11
|||||
Db 218 GAGTTGATGCTGGGCTGCAAGGACTATGAGGAG 250

RESULT 12
LOCUS RP827086
DEFINITION K-EST00004421 S9SN0601 Homo sapiens cDNA clone S9SN0601-44-609 5', mRNA sequence.
ACCESSION RP827086
VERSION RP827086.1 GI:20935634
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo 1 (bases 1 to 358)

AUTHORS

TITLE

COMMENT

Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R., Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S., and Kim, Y.S.
21C Frontier Korean EST Project 2001
Unpublished (2002)
Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong, Yuseong-gu, Daejeon 305-385, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 44 row: C column: 09
High quality sequence stop: 312.

FEATURES
source

1..312
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="S9SN0601-44-G09"
/clone_lib="S9SN0601"
/sex="M"
/tissue_type="Ascites"
/cell_type="Epithelial"
/cell_line="SNU-601"
/lab_host="Top10"
/note="Organ: Stomach; Vector: pME18-F13; Site: 1; XhoI; Site 2: XhoI; The poly (A)- RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then dephosphorylated with tabacco acid pyrophosphatase (TAP). The dephosphorylated intact mRNA was ligated with DNA-RNA linker including SfiI site by treatment of T4 RNA ligase and the first strand cDNA was synthesized with Superscript II using SfiI oligo-dT primer. After first strand synthesis, RNA was degraded by NaOH treatment and cDNA was amplified by PCR reaction. The PCR products were digested with SfiI and cloned into pTop10 digested pME18-F13 vector. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10 by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."

BASE COUNT
ORIGIN

108 a 60 c 110 q 34 l

Alignment Scores:

Pred. No.: 0.17 Length: 312
Score: 55.00 Matches: 11
Percent Similarity: 100.00%
Conservative: 0
Best Local Similarity: 100.00%
Mismatch: 0
Query Match: 100.00%
Indels: 0
DB: 14 Gaps: 0

US-09-856-070-23 (1-11) x RP827086 (1-312)

OY

1 GluLeuMetLeuArgLeuGlnAspTyrGluGlu 11
|||||

Db

218 GAGTTGATGCTGGGCTGCAAGGACTATGAGGAG 250

RESULT 12

LOCUS RP827086
DEFINITION K-EST00004421 S9SN0601 Homo sapiens cDNA clone S9SN0601-44-609 5', mRNA sequence.
ACCESSION RP827086
VERSION RP827086.1 GI:20935634
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo 1 (bases 1 to 358)

AUTHORS

Dias Neto, E., Garcia Correa, P., Verjovsky-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalha, A.F., Matsukuma, A., Hata, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jonckheere, C.V., O'Hare

REFERENCE

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo 1 (bases 1 to 358)

AUTHORS

Dias Neto, E., Garcia Correa, P., Verjovsky-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalha, A.F., Matsukuma, A., Hata, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jonckheere, C.V., O'Hare

M.J. Soares, F. Brentani, R.P. Reis, F. de Souza, S.J. and
Simpson, A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc Natl Acad Sci U S A. 97 (7), 3491-3496 (2000)
2020263
COMMENT
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICK Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?L1:CM0612-CM0-C10095-
301000-648-b05813-2000-10-30614-1)
Seq primer: puc 18 forward
High quality sequence stop: 2.
Location/Qualifiers
1 358
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="c10095"
/dev_stage="Adult"

Notes: Organ. placenta normal, Vector: puc18, Site: 1, SmaI
Site: 2, SmaI; A mini-library was made by cloning products
derived from OPSTES PCP (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions.
BASE COUNT 112 a 74 c 130 g 42 t
ORIGIN
Alignment Scores:
Prod. No.: 0 207 Length: 358
Score: 55.00 Matches: 11
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 14 Gaps: 0
US-09-856-070-23 (1-11) x BQ323637 (1-358)
QY 1 G1uLeuMetLeuArgLeuGlnAspTyrGluGlu 11
|||||
DB 231 CAGTTCATGCGCGCGCGACCTATACAGGAG 263
|||||

FEATURES

source

BASE COUNT 112 a 74 c 130 g 42 t
ORIGIN
Alignment Scores:
Prod. No.: 0 207 Length: 358
Score: 55.00 Matches: 11
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 14 Gaps: 0
US-09-856-070-23 (1-11) x BQ323637 (1-358)
QY 1 G1uLeuMetLeuArgLeuGlnAspTyrGluGlu 11
|||||
DB 231 CAGTTCATGCGCGCGCGACCTATACAGGAG 263
|||||

BASE COUNT 112 a 74 c 130 g 42 t
ORIGIN
Alignment Scores:
Prod. No.: 0 207 Length: 358
Score: 55.00 Matches: 11
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 14 Gaps: 0
US-09-856-070-23 (1-11) x BQ323637 (1-358)
QY 1 G1uLeuMetLeuArgLeuGlnAspTyrGluGlu 11
|||||
DB 231 CAGTTCATGCGCGCGCGACCTATACAGGAG 263
|||||

RESULT 13
BQ368118
LOCUS PM3-GN0516-090501-010-010 GN0516 Homo sapiens cDNA, mRNA sequence.
DEFINITION BQ368118
ACCESSION BQ368118
VERSION BQ368118.1 GI:21043632
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 364)
AUTHORS Dias Neto, E., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,
Brunstein, A., de Oliveira, P.S., Bucher, P., Jorgensen, C.V., O'Hare
M.J., Soares, F., Brentani, R.P., Reis, L.F., de Souza, S.J. and
Simpson, A.J.G.

TITLE Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
JOURNAL Proc Natl Acad Sci U S A 97 (7), 3491-3496 (2000)
MEDLINE 2020263
COMMENT Contact: Simpson A.J.G.

Laboratory of Cancer Genetics
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Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICK Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?L1:PM3-GN0516-
090501-010-010813-2001-05-09614-1)
Seq primer: puc 18 forward
High quality sequence start: 11
High quality sequence stop: 348.
Location/Qualifiers
1 364
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="GN0516"
/dev_stage="Adult"

Notes: Organ. placenta normal, Vector: puc18, Site: 1, SmaI
Site: 2, SmaI; A mini-library was made by cloning
products derived from OPSTES PCP (U.S. Letters Patent
application No. 196,716 - Ludwig Institute for Cancer
Research) profiles into the pUC 18 vector. Reverse
transcription of tissue mRNA and cDNA amplification were
performed under low stringency conditions.
BASE COUNT 112 a 64 c 146 g 42 t
ORIGIN
Alignment Scores:
Prod. No.: 0 212 Length: 364
Score: 55.00 Matches: 11
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 14 Gaps: 0
US-09-856-070-23 (1-11) x BQ368118 (1-364)
QY 1 G1uLeuMetLeuArgLeuGlnAspTyrGluGlu 11
|||||
DB 125 CAGTTCATGCGCGCGCGACCTATACAGGAG 157
|||||

RESULT 14
BQ318340/c
LOCUS BQ318340
DEFINITION M81-CT0529-140900 002 a12 CT0529 Homo sapiens cDNA, mRNA sequence.
ACCESSION BQ318340
VERSION BQ318340.1 GI:20924109
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 401)
AUTHORS Dias Neto, E., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,
Brunstein, A., de Oliveira, P.S., Bucher, P., Jorgensen, C.V., O'Hare
M.J., Soares, F., Brentani, R.P., Reis, L.F., de Souza, S.J. and
Simpson, A.J.G.

TITLE Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
JOURNAL Proc Natl Acad Sci U S A 97 (7), 3491-3496 (2000)
MEDLINE 2020263
COMMENT Contact: Simpson A.J.G.
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001

Email: asimpson@udwig.org.br
 This sequence was derived from the FAPESP/LICK Human Cancer Genome
 Project. This entry can be seen in the following URL
 (http://www.udwig.org.br/scripts/gethtml2.pl?l=MP1st2-MP1-cl00520-
 10040-m02-12474-2000-00-1454-1)

Seq primer: puc18 forward
 High quality sequence start: 2
 High quality sequence stop: 401.

FEATURES

Location/Qualifiers
 1..401
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="CT0529"
 /dev_stage="Adult"

/note="organ: colon; Vector: puc18; Site_1: Small; Site_2:
 Small; A mini-library was made by cloning products derived
 from ORIS15 PCR (U.S. Letters Patent application No. 196
 716 - Ludwig Institute for Cancer Research) profiles
 into the pUC18 vector. Reverse transcription of tissue
 mRNA and cDNA amplification were performed under low
 stringency conditions."

BASE COUNT 56 a 144 c 73 g 128 t
 ORIGIN

Alignment Scores:
 Pred. No.: 0.244 Length: 401
 Score: 55.00 Matches: 11
 Percent Similarity: 100.00% Conservat: 0
 Host Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 14 Gaps: 0

US-09-856-070-23 (1-11) x HQ318340 (1-401)

QY 1 GtGleuMctLeuArgLeuGlnAspTyrGluGlu 11

Db 249 GAGTTCATGCTGGCGTGCAGGACTATGAGGAG 217

RESULTS

15

BM744771

1400S

DEFINITION

R-EST0018496 345NT Homo sapiens cDNA clone S4SN01-18-D12 5', mRNA

sequence.

BM744771

BM744771.1 GI:19066100

EST.

SOURCE

Human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

1 (bases 1 to 404)

Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,

Oh,K.J., Choong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and

Kim,Y.S.

210 Frontier Korean EST Project 2001

Unpublished (2002)

Contact: Kim YS

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Email: yongsung@mail.kribb.re.kr

Plate: 18 row: D column: 12

High quality sequence stop: 404.

Location/Qualifiers

1..404

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="S4SN01-18-D12"

/clone_lib="S4SN01"

/sex="M"

/issue_type="Stomach"

FEATURES

source

/cell_type="Lymphoblast-like"
 /cell_line="SNU-1"
 /lab_host="top10p"

/note="organ: Stomach; Vector: pGEM1801; Site_1: EcoRI;
 Site_2: NotI; The poly (A)⁺ RNA was dephosphorylated with
 bacterial alkaline phosphatase (BAP) and then decapped
 with tobacco acid pyrophosphatase (TAP). The decapped
 intact mRNA was ligated with DNA-RNA linker including EcoR
 I site by treatment of 14 RNA ligase and the first strand
 cDNA was synthesized from oligo dt-selected mRNA by
 priming with dt-tailed vector. The dt-tailed vector was
 adjusted to have about 60nt. The cDNA vector was
 circularized with E. coli DNA ligase after digestion of
 EcoRI which site is also included in vector. An RNA strand
 converted to a DNA strand by okayama-Beck method. The
 obtained cDNA vectors were used for transformation of
 competent cells E. coli Top10p by electroporation method.
 The cDNA libraries constructed by this method are
 full-length enriched cDNA library."

BASE COUNT 127 a 83 c 141 q 53 t
 ORIGIN

Alignment Scores:

Pred. No.: 0.246 Length: 404
 Score: 55.00 Matches: 11
 Percent Similarity: 100.00% Conservat: 0
 Host Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 14 Gaps: 0

US-09-856-070-23 (1-11) x BM744771 (1-404)

QY 1 GtGleuMctLeuArgLeuGlnAspTyrGluGlu 11

Db 276 GAGTTCATGCTGGCGTGCAGGACTATGAGGAG 308

Search completed: January 16, 2003, 21:47:07
 Job time : 1455.46 secs